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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/029,495

DATE: 01/15/2002  
 TIME: 07:56:30

Input Set : A:\35905A.txt  
 Output Set: N:\CRF3\01152002\J029495.raw

ENTERED

3 <110> APPLICANT: Drmanac, Radoje T.  
 4 Labat, Ivan  
 5 Stache-Crain, Birgit  
 6 Dickson, Mark C.  
 7 Jones, Lee William  
 8 Ballinger, Dennis G.  
 9 Xue, Aidong  
 10 Tang, Y. Tom  
 11 Liu, Chenghua  
 12 Asundi, Vinod  
 14 <120> TITLE OF INVENTION: STEM CELL MAINTENANCE FACTOR MATERIALS AND METHODS  
 16 <130> FILE REFERENCE: 28110/35905A  
 18 <140> CURRENT APPLICATION NUMBER: US/10/029,495  
 19 <141> CURRENT FILING DATE: 2001-10-26  
 21 <150> PRIOR APPLICATION NUMBER: 09/378,667  
 22 <151> PRIOR FILING DATE: 1999-08-20  
 24 <150> PRIOR APPLICATION NUMBER: 09/687,527  
 25 <151> PRIOR FILING DATE: 2000-10-12  
 27 <160> NUMBER OF SEQ ID NOS: 13  
 29 <170> SOFTWARE: PatentIn Ver. 2.0  
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 32 <211> LENGTH: 560  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Homo sapiens  
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 41 <223> OTHER INFORMATION: hiwi-Hy/CG 389  
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 46 1 5 10 15  
 48 gtg stt gct cgg acc ttg aat aaa cag ggc atg atg atg agt atc gcc 97  
 W--> 49 Val Xaa Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile Ala  
 50 20 25 30  
 52 acc aag atc gct atg cag atg act tgc aag ctc gga ggc gag ctg tgg 145  
 53 Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu Trp  
 54 35 40 45  
 56 gct gtg gaa ata cct tta aag tcc ctg atg gtg gtc ggt att gat gtc 193  
 57 Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp Val  
 58 50 55 60  
 60 tgt aaa gat gca ctc agc aag gac gtg atg gtt gtt gga tgc gtg gcc 241  
 61 Cys Lys Asp Ala Leu Ser Lys Asp Val Met Val Val Gly Cys Val Ala  
 62 65 70 75 80  
 66 aqt gtt aac ccc aga atc acc agg tgg ttt tcc cgc tgt atc ctt cag 289  
 67 Ser Val Asn Pro Arg Ile Thr Arg Trp Phe Ser Arg Cys Ile Leu Gln

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68          85          90          95
70 aga aca atg act gat gtt gca gat tgc ttg aaa gtt ttc atg act gga 337
71 Arg Thr Met Thr Asp Val Ala Asp Cys Leu Lys Val Phe Met Thr Gly
72          100          105          110
74 gca ctc aac aaa tgg tac aag tac aat cat gat ttg cca gca cgg ata 385
75 Ala Leu Asn Lys Trp Tyr Lys Tyr Asn His Asp Leu Pro Ala Arg Ile
76          115          120          125
78 att gtg tac cgt gct ggt gta ggg gat ggt cag ctg aaa aca ctt att 433
79 Ile Val Tyr Arg Ala Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Ile
80          130          135          140
82 gaa tat gaa gtc cca cag ctg ctg agc agt gtg gca gaa tcc agc tca 481
83 Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser Ser
84 145          150          155          160
86 aat acc agc tca aga ctg tcg gtg att gtg gtc agg aag aag tgc atg 529
87 Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met
88          165          170          175
90 cca cga ttc ttt acc gaa atg aac cgc act g 560
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92          180          185
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98 <213> ORGANISM: Homo sapiens
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102 <222> LOCATION: (8)
103 <223> OTHER INFORMATION: Xaa = Leu
105 <220> FEATURE:
106 <221> NAME/KEY: SITE
107 <222> LOCATION: (9)
108 <223> OTHER INFORMATION: Xaa = Asp or Tyr
110 <220> FEATURE:
111 <221> NAME/KEY: SITE
112 <222> LOCATION: (18)
113 <223> OTHER INFORMATION: Xaa = Leu or Val
115 <400> SEQUENCE: 2
Wt 116 Ser Ile Lys Lys Tyr Leu Ser Xaa Xaa Cys Pro Val Pro Ser Gln Cys
117 1 5 10 15
Wt 119 Val Xaa Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile Ala
120 20 25 30
122 Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu Trp
123 35 40 45
125 Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp Val
126 50 55 60
128 Cys Lys Asp Ala Leu Ser Lys Asp Val Met Val Val Gly Cys Val Ala
129 65 70 75 80
131 Ser Val Asn Pro Arg Ile Thr Arg Trp Phe Ser Arg Cys Ile Leu Gln
132 85 90 95
134 Arg Thr Met Thr Asp Val Ala Asp Cys Leu Lys Val Phe Met Thr Gly

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135          100          105          110
137 Ala Leu Asn Lys Trp Tyr Lys Tyr Asn His Asp Leu Pro Ala Arg Ile
138          115          120          125
140 Ile Val Tyr Arg Ala Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Ile
141          130          135          140
144 Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser Ser
145 145          150          155          160
147 Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met
148          165          170          175
150 Pro Arg Phe Phe Thr Glu Met Asn Arg Thr
151          180          185
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 523
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <220> FEATURE:
160 <223> OTHER INFORMATION: hiwi
162 <400> SEQUENCE: 3
163 Gly Val Ser Phe Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile
164 1 5 10 15
166 Thr Asp Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Arg
167 20 25 30
169 Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu
170 35 40 45
172 Cys Tyr Leu Thr Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val
173 50 55 60
175 Met Lys Asp Leu Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln
176 65 70 75 80
178 Arg Glu Val Gly Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val
179 85 90 95
181 Gln Arg Glu Leu Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu
182 100 105 110
184 Ser Phe Ser Gly Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly
185 115 120 125
187 Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr
188 130 135 140
190 Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu
191 145 150 155 160
193 Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn
194 165 170 175
196 Leu Phe Lys Val Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile
197 180 185 190
199 Met Ile Glu Val Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln
200 195 200 205
202 Gln Lys Val Thr Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser
203 210 215 220
205 Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp
206 225 230 235 240
208 Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln

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209          245          250          255
211 Gln Thr Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys
212          260          265          270
214 Lys Met Gly Gly Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val
215          275          280          285
217 Met Ile Val Gly Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg
218          290          295          300
220 Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp
221 305          310          315          320
223 Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly
224          325          330          335
226 Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn
227          340          345          350
229 Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp
230          355          360          365
233 Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp
234          370          375          380
236 Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile
237 385          390          395          400
239 Val Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly
240          405          410          415
242 Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr
243          420          425          430
245 Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser
246          435          440          445
248 Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly
249          450          455          460
251 Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile
252 465          470          475          480
254 Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr
255          485          490          495
257 Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro
258          500          505          510
260 Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu
261          515          520
264 <210> SEQ ID NO: 4
265 <211> LENGTH: 866
266 <212> TYPE: PRT
267 <213> ORGANISM: Drosophila
269 <220> FEATURE:
270 <223> OTHER INFORMATION: aubergine
272 <400> SEQUENCE: 4
273 Met Asn Leu Pro Pro Asn Pro Val Ile Ala Arg Gly Arg Gly Arg Gly
274 1          5          10          15
276 Arg Lys Pro Asn Asn Val Glu Ala Asn Arg Gly Phe Ala Pro Ser Leu
277          20          25          30
279 Gly Gln Lys Ser Asp Pro Ser His Ser Glu Gly Asn Gln Ala Ser Gly
280          35          40          45
282 Gly Asn Gly Gly Gly Gly Asp Ala Gln Val Gly Pro Ser Ile Glu Lys

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## RAW SEQUENCE LISTING

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TIME 07:56:31

Input Set A:\35905A.txt

Output Set N:\CRF3\01152002\J029495.raw

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283      50      55      60
285 Ser Ser Leu Ser Ala Val Gln Met His Lys Ser Glu Gly Asp Pro Arg
286 65      70      75      80
288 Gly Ser Val Arg Gly Arg Arg Leu Ile Thr Asp Leu Val Tyr Ser Arg
289      85      90      95
291 Pro Pro Gly Met Thr Ser Lys Lys Gly Val Val Gly Thr His Ile Thr
292      100      105      110
294 Val Gln Ala Asn Tyr Phe Lys Val Leu Lys Arg Pro Asn Trp Thr Ile
295      115      120      125
297 Tyr Gln Tyr Arg Val Asp Phe Thr Pro Asp Val Glu Ala Thr Arg Leu
298      130      135      140
300 Arg Arg Ser Phe Leu Tyr Glu His Lys Gly Ile Leu Gly Gly Tyr Ile
301 145      150      155      160
303 Phe Asp Gly Thr Asn Met Phe Cys Ile Asn Gln Phe Lys Ala Val Gln
304      165      170      175
306 Asp Ser Pro Tyr Val Leu Glu Leu Val Thr Lys Ser Arg Ala Gly Glu
307      180      185      190
309 Asn Ile Glu Ile Lys Ile Lys Ala Val Gly Ser Val Gln Ser Thr Asp
310      195      200      205
312 Ala Glu Gln Phe Gln Val Leu Asn Leu Ile Leu Arg Arg Ala Met Glu
313      210      215      220
315 Gly Leu Asp Leu Lys Leu Val Ser Arg Tyr Tyr Tyr Asp Pro Gln Ala
316 225      230      235      240
318 Lys Ile Asn Leu Glu Asn Phe Arg Met Gln Leu Trp Pro Gly Tyr Gln
319      245      250      255
321 Thr Ser Ile Arg Gln His Glu Asn Asp Ile Leu Leu Cys Ser Glu Ile
322      260      265      270
324 Cys His Lys Val Met Arg Thr Glu Thr Leu Tyr Asn Ile Leu Ser Asp
325      275      280      285
327 Ala Ile Arg Asp Ser Asp Asp Tyr Gln Ser Thr Phe Lys Arg Ala Val
328      290      295      300
330 Met Gly Met Val Ile Leu Thr Asp Tyr Asn Asn Lys Thr Tyr Arg Ile
331 305      310      315      320
333 Asp Asp Val Asp Phe Gln Ser Thr Pro Leu Cys Lys Phe Lys Thr Asn
334      325      330      335
336 Asp Gly Glu Ile Ser Tyr Val Asp Tyr Tyr Lys Lys Arg Tyr Asn Ile
337      340      345      350
339 Ile Ile Arg Asp Leu Lys Gln Pro Leu Val Met Ser Arg Pro Thr Asp
340      355      360      365
343 Lys Asn Ile Arg Gly Gly Asn Asp Gln Ala Ile Met Ile Ile Pro Glu
344      370      375      380
346 Leu Ala Arg Ala Thr Gly Met Thr Asp Ala Met Arg Ala Asp Phe Arg
347 385      390      395      400
349 Thr Leu Arg Ala Met Ser Glu His Thr Arg Leu Asn Pro Asp Arg Arg
350      405      410      415
352 Ile Glu Arg Leu Arg Met Phe Asn Lys Arg Leu Lys Ser Cys Lys Gln
353      420      425      430
355 Ser Val Glu Thr Leu Lys Ser Trp Asn Ile Glu Leu Asp Ser Ala Leu
356      435      440      445

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## VERIFICATION SUMMARY

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Input Set : A:\35905A.txt

Output Set: N:\CRF3\01152002\J029495.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2